

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 7, 2002, 16:03:54 ; Search time 180.87 Seconds
(without alignments)
38.818 Million cell updates/sec

Title: US-08-569-749-10

Perfect score: 294

Sequence: 1 PEQLASAGFYVGNSDYKC.....CWESGDDPMVQHAKKFPKCE 48

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	294	100.0	1140 4 Q9UWH1	Q9UWH1 homo sapien
2	277	94.2	195 13 Q91A70	Q91A70 gallus galli
3	277	94.2	197 13 Q91A69	Q91A69 gallus galli
4	277	94.2	610 13 Q91A70	Q91A70 gallus galli
5	276	93.9	602 11 Q91A69	Q91A69 gallus galli
6	270	91.8	589 11 Q91A69	Q91A69 gallus galli
7	270	91.8	589 11 Q91A69	Q91A69 gallus galli
8	258	87.8	324 13 Q91A69	Q91A69 gallus galli
9	205	69.7	224 11 Q91A69	Q91A69 gallus galli
10	202	68.7	264 12 Q91A69	Q91A69 gallus galli
11	193	65.6	280 4 Q91A69	Q91A69 gallus galli
12	193	65.6	281 12 Q91A69	Q91A69 gallus galli
13	193	65.6	288 4 Q91A69	Q91A69 gallus galli
14	191	65.0	276 12 Q91A69	Q91A69 gallus galli
15	191	65.0	379 5 Q91A69	Q91A69 gallus galli
16	190	64.6	377 5 Q91A69	Q91A69 gallus galli
17	180	61.2	597 11 Q91A69	Q91A69 gallus galli
18	177	60.2	496 11 Q91A69	Q91A69 gallus galli
19	177	60.2	501 11 Q91A69	Q91A69 gallus galli

20	177	60.2	501	11	Q91A69	Q91A69 gallus galli
21	173	58.8	313	12	Q91A69	Q91A69 gallus galli
22	169	57.5	261	12	Q91A69	Q91A69 gallus galli
23	163	55.4	438	5	Q91A69	Q91A69 gallus galli
24	125	42.5	268	12	Q91A69	Q91A69 gallus galli
25	125	42.5	268	12	Q91A69	Q91A69 gallus galli
26	123.5	42.0	4904	5	Q91A69	Q91A69 gallus galli
27	122.5	41.7	153	5	Q91A69	Q91A69 gallus galli
28	116.5	39.6	4845	11	Q91A69	Q91A69 gallus galli
29	116	39.5	150	12	Q91A69	Q91A69 gallus galli
30	111	37.8	292	12	Q91A69	Q91A69 gallus galli
31	107	36.4	208	12	Q91A69	Q91A69 gallus galli
32	102.5	34.9	301	12	Q91A69	Q91A69 gallus galli
33	102	34.7	284	12	Q91A69	Q91A69 gallus galli
34	93	31.6	155	12	Q91A69	Q91A69 gallus galli
35	92.5	31.5	142	13	Q91A69	Q91A69 gallus galli
36	92.5	31.5	285	12	Q91A69	Q91A69 gallus galli
37	86.5	29.4	142	6	Q91A69	Q91A69 gallus galli
38	81.5	27.7	187	12	Q91A69	Q91A69 gallus galli
39	80	27.2	306	5	Q91A69	Q91A69 gallus galli
40	77	26.2	87	11	Q91A69	Q91A69 gallus galli
41	76	25.9	87	11	Q91A69	Q91A69 gallus galli
42	76	25.9	137	4	Q91A69	Q91A69 gallus galli
43	75	25.5	155	5	Q91A69	Q91A69 gallus galli
44	75	25.5	87	11	Q91A69	Q91A69 gallus galli
45	75	25.5	281	12	Q91A69	Q91A69 gallus galli

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	1140 AA.
Q9UWH1	Q9UWH1			
AC	Q9UWH1			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	API2-MLT FUSION PROTEIN.			
GN	API2-MLT.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-99272400; PubMed-10339464;			
RA	Hernandez J.M., Baens M., Wlodarska T., Stefanova-Ouzounova M.,			
RA	Van den Bergh H., Hossfeld D.K., De Wolf-Peters C., Hagemeijer A.,			
RT	"The apoptosis inhibitor gene API2 and a novel 18k gene, MT, are			
RT	recurrently rearranged in the t(11;18)(q21;q21) associated with			
RT	muscle associated lymphoid tissue lymphomas."			
RL	Blood 93:3601-3609 (1993).			
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN.			
DR	EMBL: AF123094; AAD46161.1; -			
DR	HSSP: Q13490; IQBH.			
DR	InterPro: IPR001370; BIR.			
DR	InterPro: IPR003576; Caspase.			
DR	InterPro: IPR001309; ICE_P20.			
DR	InterPro: IPR003588; IG_C2.			
DR	InterPro: IPR003600; IG_Like.			
DR	InterPro: IPR003006; IG_MHC.			
DR	Pfam: PF00653; BIR; 3.			
DR	Pfam: PF00047; Iq; 2.			
DR	SMART: SM00238; BIR; 3.			
DR	SMART: SM00115; CASC; 1.			
DR	SMART: SM00408; ICE2; 1.			
DR	SMART: SM00410; IG_Like; 1.			
DR	PROSITE: PS01282; BIR_REPEAT_1; 3.			
DR	PROSITE: PS0143; BIR_REPEAT_2; 3.			
DR	PROSITE: PS0208; CASPASE_P20; 1.			

PT REPEAT 262 329 BIR REPEAT 3.
RT ZN-FING 563 597 C3HC4-TYPE.
SQ SEQUENCE 610 AA; 68924 MW; ADP47619650B44AC CRC64;

Query Match 94.2%; Score 277; DB 13; Length 610;
Best Local Similarity 89.6%; Pred. No. 2.9e-28;
Matches 43; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGNSDVYKFCFCCDGLRCWESGDDPWVGHAKWPRCE 48
DB 280 PEOLASAGFYVGNSDVYKFCFCCDGLRCWESGDDPWVGHAKWPRCE 327

RESULT 5
Q9ES69 PRELIMINARY; PRT; 602 AA.
AC Q9ES69;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF183430; AAC22970.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; ZF-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR SMART: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR Zinc-finger.
KW SEQUENCE 602 AA; 67326 MW; CC91385E6A2DE5A CRC64;
SO SEQUENCE

Query Match 93.9%; Score 276; DB 11; Length 602;
Best Local Similarity 89.6%; Pred. No. 3.9e-28;
Matches 43; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGNSDVYKFCFCCDGLRCWESGDDPWVGHAKWPRCE 48
DB 273 PEOLASAGFYVGNSDVYKFCFCCDGLRCWESGDDPWVGHAKWPRCE 320

RESULT 6
Q9QZC6 PRELIMINARY; PRT; 569 AA.
AC Q9QZC6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE-KIDNEY;
RA Dong Z., Denton M., Gu S.M., Saikumar P., Venkatchalam M.A.;
RT "Cloning of cDNA for rat inhibitor of apoptosis protein 2."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF190020; AAC04585.1; -.
DR HSSP: O13490; IOBH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; ZF-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR Zinc-finger.
KW SEQUENCE 589 AA; 66777 MW; E6812FEE3EA3142 CRC64;
SO SEQUENCE

Query Match 91.8%; Score 270; DB 11; Length 589;
Best Local Similarity 87.5%; Pred. No. 2.4e-27;
Matches 42; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGNSDVYKFCFCCDGLRCWESGDDPWVGHAKWPRCE 48
DB 259 PEOLASAGFYVGNSDVYKFCFCCDGLRCWESGDDPWVGHAKWPRCE 306

RESULT 7
Q9ES68 PRELIMINARY; PRT; 589 AA.
AC Q9ES68;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN 2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Holcik M., Lefebvre C.A., Hicks K., Korneluk R.G.;
RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of
RT Apoptosis Protein 1, 2, and 3 Genes."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL: AF183431; AAC22971.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; ZF-C3HC4; 1.
DR Pfam: PF00038; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
DR Zinc-finger.
KW SEQUENCE 589 AA; 66750 MW; BA47089AD7CD285B CRC64;
SO SEQUENCE

Query Match 91.8%; Score 270; DB 11; Length 589;
Best Local Similarity 87.5%; Pred. No. 2.4e-27;
Matches 42; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGNSDVYKFCFCCDGLRCWESGDDPWVGHAKWPRCE 48

Db 259 PEOLASAGFYVDHNDVKCFCCDGLRCWCFPGDDPWIGHAKWFRCE 306

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RESULT 8
OQ9DNN2 ID Q9DNN2 PRELIMINARY: PRT: 324 AA.
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE APOPTOSIS INHIBITOR CH-1A1 (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Pendleton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;
RT "The apoptosis inhibitor ch-1A1 is a direct transcriptional target of
RT v-Rel and c-Rel."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF311289; AAC42316.1; -.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 3.
DR SMART: SM00238; BIR; 3.
DR PROSITE: PS01282; BIR_REPEAT_1; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
FT NON_TER 324
SQ SEQUENCE 324 AA: 36567 MW; 5E2B89DEAE373AF3 CRC64;

```

Query Match 87.8%; Score 258; DB 13; Length 324;
 Best Local Similarity 88.9%; Pred. No. 4.8e-26;
 Matches 40; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGNSDYKCFCCDGLRCWESGDDPWIGHAKWMP 45
 Db 280 PEOLADAGFYVGRNDVKCFCCDGLRCWESGDDPWIGHAKWMP 324

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RESULT 9
OQ8642 ID Q8642 PRELIMINARY: PRT: 224 AA.
AC O8642.
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
GN RIAP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-WISTAR; TISSUE-OVARY; CORPUS LUTEUM;
RA Bradley C.K., Lareu R.R., Dharmarajan A.M.;
RT "Cloning and characterisation of an inhibitor of apoptosis protein
RT (IAP) in the rat corpus luteum."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF081503; AAC32497.1; -.
DR HSP: Q13490; IOBH.
DR InterPro: IPR001370; BIR.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
FT NON_TER 224
SQ SEQUENCE 224 AA: 25209 MW; 213A52534D5EB56A CRC64;

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Query Match 69.7%; Score 205; DB 11; Length 224;
 Best Local Similarity 89.2%; Pred. No. 3.1e-19;
 Matches 33; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PEOLASAGFYVGNSDYKCFCCDGLRCWESGDDPW 37
 Db 188 PEOLASAGFYVDHNDVKCFCCDGLRCWESGDDPW 224

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RESULT 10
OQ9EN27 ID Q9EN27 PRELIMINARY: PRT: 264 AA.
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE AWO21.
GN AWO21.
OS Amsacta moorei entomopoxvirus (AmpPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
OC Entomopoxvirus B.
OX NCBI_TaxID=28321;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20396580; PubMed-10936094;
RA Bowden A.L., Glassberg K.J., Digians J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RT "Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
RT Analysis and Comparison with Other Poxviruses."
RL Virology 274:120-139(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Bowden A.L., Glassberg K.J., Digians J., Shaw R., Farmerie W.,
RA Moyer R.W.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF250284; AAC02727.1; -.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00653; BIR; 2.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
SQ SEQUENCE 264 AA: 30547 MW; 2EB72DA4B5BD920A CRC64;

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Query Match 68.7%; Score 202; DB 12; Length 264;
 Best Local Similarity 66.0%; Pred. No. 9e-19; 9; Indels 0; Gaps 0;
 Matches 31; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

OY 2 EOLASAGFYVGNSDYKCFCCDGLRCWESGDDPWIGHAKWFRCE 48
 Db 126 EKLAEAGFYTKSDYKCFCCDGLRCWETDDPWIGHAKWFRCD 172

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RESULT 11
OQ9HAP7 ID Q9HAP7 PRELIMINARY: PRT: 280 AA.
AC Q9HAP7.
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE LYTIN INHIBITOR OF APOPTOSIS (INHIBITOR OF APOPTOSIS) (BA261N11.1.1)
DE (BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 7 (LYTIN), ISOFORM 1).
GN LYTIN OR BIC7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kasof G.M., Gomes B.C.;
RT "Lytn, a novel inhibitor-of-apoptosis (IAP) family member."
RL J. Biol. Chem. 0:0-0(2000).

```

[2]
 RP SEQUENCE FROM N.A.
 RA Ashbab Y., Allan A., Pollack A., Panet A., Ben-Yehuda D.;
 RT "Two splicing variants of a new inhibitor of apoptosis gene with
 RL different biological properties and tissue distribution pattern."
 RL submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
 CC EMBL: AF311368; AAC33622.1; -
 DR EMBL: AJ309298; CAC37337.1; -
 DR EMBL: AL121827; CAC36112.1; -
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001841; znf_ring.
 DR Pfam: PF00653; BIR; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS50143; BIR_REPEAT_2; 1.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; UNKNOWN_1.
 DR Zinc-finger.
 KW
 SO SEQUENCE 280 AA; 30866 MW; 630BE9C0737F952 CRC64;

Query Match 65.6%; Score 193; DB 4; Length 280;
 Best Local Similarity 60.4%; Pred. No. 1.5e-17;
 Matches 29; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Oy 1 PQLASAGFYVGNSSDDVKGCCGCGGCLRCWESGDDPWVQHAKEPRCE 48
 Db 105 PQLAAGFFHTGHQDKVRCFCYGGIQLQSMKRGDDPWVTHAKWPSQ 152

RESULT 12
 ID 09YNL8 PRELIMINARY; PRT; 281 AA.
 AC 09YNL8;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE IAP PROTEIN.
 GN IAP.
 OS Chortstoneura famiferana nuclear polyhedrosis virus (CTMPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 CC Nucleopolyhedrovirus.
 CX NCBI_TaxId=10448;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=IRELAND;
 RA Lauzon H., Arlet B.M., Ladd T., Palli R.;
 RT "CTMPV IAP gene."
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
 DR EMBL: U82510; AAD00537.1; -
 DR HSP; Q13490; 10BH.
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001841; znf_ring.
 DR Pfam: PF00653; BIR; 2.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 2.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01282; BIR_REPEAT_1; UNKNOWN_1.
 DR PROSITE: PS01443; BIR_REPEAT_2; 2.
 DR Zinc-finger.
 KW
 SO SEQUENCE 281 AA; 32090 MW; B2D9BE8A359F105E CRC64;

Query Match 65.6%; Score 193; DB 12; Length 281;
 Best Local Similarity 68.1%; Pred. No. 1.5e-17;
 Matches 32; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Oy 1 PQLASAGFYVGNSSDDVKGCCGCGGCLRCWESGDDPWVQHAKEPRC 47
 Db 142 PQLAAGFFHTGHQDKVRCFCYGGIQLQSMKRGDDPWVTHAKWPSQ 188

RESULT 13
 ID 09H2A8 PRELIMINARY; PRT; 298 AA.
 AC 09H2A8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE INHIBITOR OF APOPTOSIS PROTEIN KIAA (BA261N11.1-2) (BACULOVIRAL IAP
 DE REPEAT-CONTAINING PROTEIN 7 (LITVIN), ISOFORM 2).
 GN BIRC7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RA Lin J.-H., Deng G., Huang Q., Morser J.;
 RT "A novel member of the inhibitor of apoptosis protein family."
 RL Biochem. Biophys. Res. Commun. 0:0-0(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ashbab Y., Allan A., Pollack A., Panet A., Ben-Yehuda D.;
 RT "Two splicing variants of a new inhibitor of apoptosis gene with
 RL different biological properties and tissue distribution pattern."
 RL submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
 CC EMBL: AF301009; AAC37878.1; -
 DR EMBL: AJ309298; CAC37338.1; -
 DR EMBL: AL121827; CAC36111.1; -
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001841; znf_ring.
 DR Pfam: PF00653; BIR; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00238; BIR; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS50143; BIR_REPEAT_2; 1.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; UNKNOWN_1.
 DR Zinc-finger.
 KW
 SO SEQUENCE 298 AA; 32798 MW; B2EAAE531BEC101 CRC64;

Query Match 65.6%; Score 193; DB 4; Length 298;
 Best Local Similarity 60.4%; Pred. No. 1.6e-17;
 Matches 29; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Oy 1 PQLASAGFYVGNSSDDVKGCCGCGGCLRCWESGDDPWVQHAKEPRCE 48
 Db 105 PQLAAGFFHTGHQDKVRCFCYGGIQLQSMKRGDDPWVTHAKWPSQ 152

RESULT 14
 ID 089744 PRELIMINARY; PRT; 276 AA.
 AC 089744;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE APOPTOSIS INHIBITOR IAP-1.
 GN IAP1.
 OS Buzura suppressaria nuclear polyhedrosis virus (BsnPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 CC Nucleopolyhedrovirus.
 CX NCBI_TaxId=74520;

Search completed: January 7, 2002, 16:03:54
Job time: 1413 sec

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RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE-9637635; PubMed-9712513;
RA Hu Z.H., Arlt B.M., Sun J.S., Chen X.W., Zuidema D., Goldbach R.W.,
RA Vlak J.M.;
RT "Genetic organization of the HindIII-E region of the single-
RT nucleocapsid nucleopolydiovirus of Buzura suppressaria.";
RL Virus Res. 55:71-82(1998).
CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR EMBL; AF045936; AAC34373.1; -.
DR HSSP; Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00653; BIR; 2.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
RM Zinc-finger.
SQ
SEQUENCE 276 AA; 31617 MW; C467275E58D36422 CRC64;

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Query Match 65.0%; Score 191; DB 12; Length 276;
Best Local Similarity 63.8%; Pred. No. 2,6e-17;
Matches 30; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

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OY 1 PROLASAGFYVGNSDVKFCFCDDGLRCWESGDDPWVQAKWPPRC 47
DB 127 PEGLDAGCFYTGSDKTCFCNGGLKDWEDGDEPMEQAHWFDC 173

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RESULT 15
O90492 PRELIMINARY; PRT; 379 AA.
ID O90492;
AC O90492;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN.
GN IAP1.
OS Trichoplusia ni (Cabbage looper).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuidae; Noctuidae; Plusiinae; Trichoplusia.
OX NCBI_TaxID=7111;
RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE-20062908; PubMed-10593985;
RA Seshagiri S., Vucic D., Lee J., Dixit V.M.;
RT "Baculovirus-based genetic screen for antileptotic genes identifies a
RT novel IAP.";
RL J. Biol. Chem. 274:36769-36773(1999).
DR EMBL; AF195528; AAF19819.1; -.
DR HSSP; Q13490; 10BH.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
SQ
SEQUENCE 379 AA; 41857 MW; 069381A012D9DE65 CRC64;

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Query Match 65.0%; Score 191; DB 5; Length 379;
Best Local Similarity 63.8%; Pred. No. 3,7e-17;
Matches 30; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

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OY 1 PROLASAGFYVGNSDVKFCFCDDGLRCWESGDDPWVQAKWPPRC 47
DB 227 PEGLDAGCFYTGSDKTCFCNGGLKDWEDGDEPMEQAHWFDC 273

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